10/045,631

(FILE 'HOME' ENTERED AT 14:59:52 ON 26 MAR 2004)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004

L1	13661	S	KINESIN
L2	2217	S	HUMAN AND L1
L3	3637	S	"MOTOR DOMAIN?"
L4	328	S	L2 AND L3
L5	777	S	"CENP-E"
L6	12	S	L4 AND L5
L7	5	DUP REM	L6 (7 DUPLICATES REMOVED)
L8	74	S	"CENTROMERE-ASSOCIATED PROTEIN-E"
L9	34	S	HUMAN AND L8
L10	29	DUP REM	L9 (5 DUPLICATES REMOVED)
L11	0	S	"UNGLYCOSYLAT"
L12	4821	S	UNGLYCOSYLATED
L13	778	S	L10 OR L5
L14	1	S	L12 AND L13
		E	BERAUD C/AU
L15	473	S	E3
		E	OHASHI C/AU
L16	55	S	E3-E7
		E	SAKOWICZ R/AU
L17	68	S	E5
		E	VAISBERG E/AU
L18	15	S	E12
		E	WOOD K/AU
L19	781	S	E3
		E	YU M/AU
L20	2239	S	E3
		E	BERAUD C
		E	BERAUD C/AU
L21	114	S	E9
		E	L2 OR L3
L22	3237	S	L16 OR L17 OR L18 OR L19 OR L20 OR L21
L23	6	S	L13 AND L22
L24	5	DUP REM	L23 (1 DUPLICATE REMOVED)

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                   present
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 NEWS 10  DEC 08   CABA reloaded with left truncation
 NEWS 11  DEC 08   IMS file names changed
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                   in REGISTRY
 NEWS 13  DEC 09   STN Entry Date available for display in REGISTRY and CA/CAplus
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 NEWS 15  DEC 18   BIOTECHNO no longer updated
 NEWS 16  DEC 19   CROPU no longer updated; subscriber discount no longer
                   available
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                   databases
 NEWS 18  DEC 22   IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields
 NEWS 19  DEC 22   ABI-INFORM now available on STN
 NEWS 20  JAN 27   Source of Registration (SR) information in REGISTRY updated
                   and searchable
 NEWS 21  JAN 27   A new search aid, the Company Name Thesaurus, available in
                   CA/CAplus
 NEWS 22  FEB 05   German (DE) application and patent publication number format
                   changes
 NEWS 23  MAR 03   MEDLINE and LMEDLINE reloaded
 NEWS 24  MAR 03   MEDLINE file segment of TOXCENTER reloaded
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               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 3 MARCH 2004
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=> file medline embase biosis biotechds scisearch hcaplus ntis lifesci
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FILE 'LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004
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=> s kinesin
L1       13661 KINESIN

=> s human and l1
L2        2217 HUMAN AND L1

=> s "motor domain?"
L3        3637 "MOTOR DOMAIN?"

=> s l2 and l3
L4         328 L2 AND L3

=> s "CENP-E"
L5         777 "CENP-E"

=> s l4 and l5
L6          12 L4 AND L5

=> dup rem l6
PROCESSING COMPLETED FOR L6
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)

=> d 1-5 ibib ab
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L7 ANSWER 1 OF 5 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2001688509 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11734897
TITLE: Maximum likelihood methods reveal conservation of function among closely related **kinesin** families.
AUTHOR: Lawrence Carolyn J; Malmberg Russell L; Muszynski Michael G; Dawe R Kelly
CORPORATE SOURCE: University of Georgia, Department of Botany, Athens, GA 30602, USA.
SOURCE: Journal of molecular evolution, (2002 Jan) 54 (1) 42-53. Journal code: 0360051. ISSN: 0022-2844.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20011206
Last Updated on STN: 20020816
Entered Medline: 20020815

AB We have reconstructed the evolution of the anciently derived **kinesin** superfamily using various alignment and tree-building methods. In addition to classifying previously described **kinesins** from protists, fungi, and animals, we analyzed a variety of **kinesin** sequences from the plant kingdom including 12 from Zea mays and 29 from Arabidopsis thaliana. Also included in our data set were four sequences from the anciently diverged amitochondriate protist Giardia lamblia. The overall topology of the best tree we found is more likely than previously reported topologies and allows us to make the following new observations: (1) **kinesins** involved in chromosome movement including MCAK, chromokinesin, and **CENP-E** may be descended from a single ancestor; (2) **kinesins** that form complex oligomers are limited to a monophyletic group of families; (3) **kinesins** that crosslink antiparallel microtubules at the spindle midzone including BIMC, MKLP, and **CENP-E** are closely related; (4) Drosophila NOD and **human** KID group with other characterized chromokinesins; and (5) Saccharomyces SMY1 groups with **kinesin**-I sequences, forming a family of **kinesins** capable of class V myosin interactions. In addition, we found that one monophyletic clade composed exclusively of sequences with a C-terminal **motor domain** contains all known minus end-directed **kinesins**.

L7 ANSWER 2 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 1998:437989 SCISEARCH
THE GENUINE ARTICLE: ZR489
TITLE: Rigor-type mutation in the **kinesin**-related protein HsEg5 changes its subcellular localization and induces microtubule bundling
AUTHOR: Blangy A (Reprint); Chaussepied P; Nigg E A
CORPORATE SOURCE: CNRS, CRBM, IFR 24, 1919 ROUTE MENDE, F-34033 MONTPELLIER, FRANCE (Reprint); SWISS INST EXPT CANC RES, CH-1066 EPALINGES, SWITZERLAND; UNIV GENEVA, DEPT MOL BIOL, CH-1211 GENEVA, SWITZERLAND
COUNTRY OF AUTHOR: FRANCE; SWITZERLAND
SOURCE: CELL MOTILITY AND THE CYTOSKELETON, (FEB 1998) Vol. 40, No. 2, pp. 174-182.
Publisher: WILEY-LISS, DIV JOHN WILEY & SONS INC, 605 THIRD AVE, NEW YORK, NY 10158-0012.
ISSN: 0886-1544.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 54
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB HsEg5 is a **human kinesin**-related motor protein essential for the formation of a bipolar mitotic spindle. It interacts with the mitotic centrosomes in a phosphorylation-dependent manner. To investigate further the mechanisms involved in targetting HsEg5 to the spindle apparatus, we expressed various mutants of HsEg5 in HeLa cells. All these mutants share a mutation of Thr-112 in the N-terminal **motor domain**, resulting in the inactivation of the ATP binding domain. In vitro, the HsEg5-T112N mutant **motor domain** showed a nucleotide-independent microtubule association, typical of a **kinesin** protein binding to microtubules in a rigor state. In vivo, overexpression of the HsEg5 rigor mutant in HeLa cells induced, in interphase, microtubule bundling, and, in mitosis, the formation of monopolar mitotic spindles similar to those observed after microinjection of anti-HsEg5 antibodies. Localization of the HsEg5 rigor mutant on cytoplasmic microtubules did not require the C-terminal tail domain but was lost when the stalk domain was also deleted. Sucrose gradient centrifugation experiments showed that microtubule bundling was most likely caused by the binding of HsEg5 mutants in a dimeric state. These results demonstrate that the precise subcellular localization of HsEg5 in vivo is regulated not only by the phosphorylation of the tail domain but also by the oligomeric state of the protein. (C) 1998 Wiley-Liss, Inc.

L7 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 1998060834 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9396744
TITLE: **CENP-E** function at kinetochores is essential for chromosome alignment.
AUTHOR: Schaar B T; Chan G K; Maddox P; Salmon E D; Yen T J
CORPORATE SOURCE: Cell and Molecular Biology Graduate Group, University of Pennsylvania, Philadelphia, Pennsylvania 19103, USA.
CONTRACT NUMBER: CA06927 (NCI)
GM24364 (NIGMS)
GM44762 (NIGMS)
SOURCE: Journal of cell biology, (1997 Dec 15) 139 (6) 1373-82.
Journal code: 0375356. ISSN: 0021-9525.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980129
Last Updated on STN: 19980129
Entered Medline: 19980113

AB **CENP-E** is a **kinesin**-like protein that binds to kinetochores and may provide functions that are critical for normal chromosome motility during mitosis. To directly test the in vivo function of **CENP-E**, we microinjected affinity-purified antibodies to block the assembly of **CENP-E** onto kinetochores and then examined the behavior of these chromosomes. Chromosomes lacking **CENP-E** at their kinetochores consistently exhibited two types of defects that blocked their alignment at the spindle equator. Chromosomes positioned near a pole remained mono-oriented as they were unable to establish bipolar microtubule connections with the opposite pole. Chromosomes within the spindle established bipolar connections that supported oscillations and normal velocities of kinetochore movement between the poles, but these bipolar connections were defective because they failed to align the chromosomes into a metaphase plate. Overexpression of a mutant that lacked the amino-terminal 803 amino acids of **CENP-E** was found to saturate limiting binding sites on kinetochores and competitively blocked endogenous **CENP-E** from assembling onto kinetochores. Chromosomes saturated with the truncated **CENP-E** mutant were never found to be aligned but accumulated at the poles or were strewn

within the spindle as was the case when cells were microinjected with **CENP-E** antibodies. As the **motor domain** was contained within the portion of **CENP-E** that was deleted, the chromosomal defect is likely attributed to the loss of motor function. The combined data show that **CENP-E** provides kinetochore functions that are essential for monopolar chromosomes to establish bipolar connections and for chromosomes with connections to both spindle poles to align at the spindle equator. Both of these events rely on activities that are provided by **CENP-E's motor domain**.

L7 ANSWER 4 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 95:329093 SCISEARCH
THE GENUINE ARTICLE: QY118
TITLE: CHARACTERIZATION OF A MINUS END-DIRECTED **KINESIN**-LIKE MOTOR PROTEIN FROM CULTURED-MAMMALIAN-CELLS
AUTHOR: KURIYAMA R (Reprint); KOFRON M; ESSNER R; KATO T; DRAGASGRANOIC S; OMOTO C K; KHODJAKOV A
CORPORATE SOURCE: UNIV MINNESOTA, DEPT CELL BIOL & NEUROANAT, 4-135 JACKSON HALL, 321 CHURCH ST SE, MINNEAPOLIS, MN, 55455 (Reprint); WASHINGTON STATE UNIV, DEPT GENET & CELL BIOL, PULLMAN, WA, 99164
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF CELL BIOLOGY, (MAY 1995) Vol. 129, No. 4, pp. 1049-1059.
ISSN: 0021-9525.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 51

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Using the CHO2 monoclonal antibody raised against CHO spindles (Sellitto, C., M. Kimble, and R. Kuriyama. 1992. Cell Motil. Cytoskeleton. 22:7-24) we identified a 66-kD protein located at the interphase centrosome and mitotic spindle. Isolated cDNAs for the antigen encode a 622-amino acid polypeptide. Sequence analysis revealed the presence of 340-amino acid residues in the COOH terminus, which is homologous to the **motor domain** conserved among other members of the **kinesin** superfamily. The protein is composed of a central alpha-helical portion with globular domains at both NH2 and COOH termini, and the epitope to the monoclonal antibody resides in the central alpha-helical stalk. A series of deletion constructs were created for in vitro analysis of microtubule interactions. While the microtubule binding and bundling activities require both the presence of the COOH terminus and the alpha-helical domain, the NH2-terminal half of the antigen lacked the ability to interact with microtubules. The full-length as well as deleted proteins consisting of the COOH-terminal motor and the central alpha-helical stalk supported microtubule gliding, with velocity ranging from 1.0 to 8.4 mu m/minute. The speed of microtubule movement decreased with decreasing lengths of the central stalk attached to the COOH-terminal motor. The microtubules moved with their plus end leading, indicating that the antigen is a minus end-directed motor. The CHO2 sequence shows 86% identify to HSET, a gene located at the centromeric end of the **human** MHC region in chromosome 6 (Ando, A., Y. Y. Kikuti, H. Kawata, N. Okamoto, T. Imai, T. Eki, K. Yokoyama, E. Soeda, T. Ikemura, K. Abe, and H. Inoko. 1994. Immunogenetics. 39:194-200), indicating that HSET might represent a **human** homologue of the CHO2 antigen.

L7 ANSWER 5 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 95:65950 SCISEARCH
THE GENUINE ARTICLE: QB175
TITLE: HETEROGENEITY AND MICROTUBULE INTERACTION OF THE CHO1 ANTIGEN, A MITOSIS-SPECIFIC **KINESIN**-LIKE PROTEIN - ANALYSIS OF SUBDOMAINS EXPRESSED IN INSECT SF9 CELLS

AUTHOR: KURIYAMA R (Reprint); DRAGASGRANOIC S; MAEKAWA T; VASSILEV A; KHODJAKOV A; KOBAYASHI H
CORPORATE SOURCE: UNIV MINNESOTA, DEPT CELL BIOL & NEUROANAT, 4-135 JACKSON HALL, 321 CHURCH ST SE, MINNEAPOLIS, MN, 55455 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF CELL SCIENCE, (DEC 1994) Vol. 107, Part 12, pp. 3485-3499.
ISSN: 0021-9533.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 52

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The CHO1 antigen is a mitosis-specific **kinesin**-like motor located at the interzonal region of the spindle. The **human** cDNA coding for the antigen contains a domain with sequence similarity to the **motor domain** of **kinesin**-like protein (Nislow et al., Nature 359, 543, 1992). Here we cloned cDNAs encoding the CHO1 antigen by immunoscreening of a CHO Uni-Zap expression library, the same species in which the original monoclonal antibody was raised, cDNAs of CHO cells encode a 953 amino acid polypeptide with a calculated molecular mass of 109 kDa. The N-terminal 73% of the antigen was 87% identical to the **human** clone, whereas the remaining 27% of the coding region showed only 48% homology. Insect Sf9 cells infected with baculovirus containing the full-length insert produced 105 and 95 kDa polypeptides, the same doublet identified as the original antigen in CHO cells. Truncated polypeptides corresponding to the N-terminal motor and C-terminal tail produced a 56 and 54 kDa polypeptide in Sf9 cells, respectively. Full and N-terminal proteins co-sedimented with, and caused bundling of, brain microtubules in vitro, whereas the C-terminal polypeptide did not. Cells expressing the N terminus formed one or more cytoplasmic processes. Immunofluorescence as well as electron microscopic observations revealed the presence of thick bundles of microtubules, which were closely packed, forming a marginal ring just beneath the cell membrane and a core in the processes. The diffusion coefficient and sedimentation coefficient were determined for the native CHO1 antigen by gel filtration and sucrose density gradient centrifugation, respectively. The native molecular mass of overinduced protein in Sf9 cells was calculated as 219 kDa, suggesting that the antigen exists as a dimer. Intrinsic CHO1 antigen in cultured mammalian cells forms a larger native complex (native molecular mass, 362 kDa), which may suggest the presence of additional molecule(s) associating with the CHO1 motor molecule.

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     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004
L1         13661 S KINESIN
L2          2217 S HUMAN AND L1
L3          3637 S "MOTOR DOMAIN?"
L4           328 S L2 AND L3
L5           777 S "CENP-E"
L6            12 S L4 AND L5
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)

=> s "centromere-associated protein-E"
L8            74 "CENTROMERE-ASSOCIATED PROTEIN-E"

=> s human and l8
L9            34 HUMAN AND L8
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=> dup rem l9
PROCESSING COMPLETED FOR L9
L10          29 DUP REM L9 (5 DUPLICATES REMOVED)

=> d 1-29 ibib ab

L10  ANSWER 1 OF 29  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2003:1006806  HCAPLUS
DOCUMENT NUMBER:          140:53394
TITLE:                    Use of HEC1 antagonists in the treatment of
                          proliferative disorders and cancer
INVENTOR(S):              Nigg, Erich A.; Martin-Lluesma, Silvia; Stucke, Volker
PATENT ASSIGNEE(S):       Max-Planck-Gesellschaft Zur Foerderung Der
                          Wissenschaften E.V., Germany
SOURCE:                   PCT Int. Appl., 58 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
     WO 2003105891      A2   20031224       WO 2003-EP6205   20030612
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
             PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT,
             TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,
             MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
             NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
             GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                  EP 2002-13006    A  20020612
AB   The present invention relates to the use of (an) anti-HEC1 compound(s), (an)
     HEC1-complex antagonist(s) and/or (an) HEC1-complex inhibitor(s) for the
     preparation of a pharmaceutical composition for the prevention, amelioration
and/or
     prevention of a hyperproliferative disorder/disease.  Furthermore, the
     invention provides for a pharmaceutical composition comprising at least one
     anti-HEC1 compound, at least one HEC1-complex antagonist and/or at least one
     HEC1-complex inhibitor.  Addnl., the invention relates to a method for
     identifying an anti-Hec1 compound, an HEC1-complex antagonist or an
     HEC1-complex inhibitor.

L10  ANSWER 2 OF 29  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2003:837370  HCAPLUS
DOCUMENT NUMBER:          139:333972
TITLE:                    Gene profiling methods of diagnosing potential for
                          metastasis or developing hepatocellular carcinoma and
                          of identifying therapeutic targets
INVENTOR(S):              Wang, Xin Wei; Ye, Qing-hai; Kim, Jin Woo
PATENT ASSIGNEE(S):       The Government of the United States of America, as
                          Represented by the Secretary of the Department of
                          Health and Human Services, USA
SOURCE:                   PCT Int. Appl., 141 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:
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PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003087766	A2	20031023	WO 2003-US10783	20030404

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-370895P P 20020405

AB The present invention relates to methods for diagnosing the metastatic potential of hepatocellular carcinoma (HCC) in HCC patients and methods for diagnosing the potential of developing HCC in patients with chronic liver diseases. A computer readable medium, a digital computer, and a system useful for such diagnosis are also provided. Further disclosed are methods for identifying potential therapeutic targets for treating metastasis in HCC patients and methods for preventing HCC in patients with chronic liver diseases. Based on UniGene (UG) database compiled by NCBI, two sets of gene clusters: Metastatic gene expression predictor correlated with the diagnosis of metastatic HCC and HCC gene expression predictor correlated with the diagnosis of patients likely to develop HCC, are identified by gene profiling method. Among them, osteopontin (OPN) and EpCAM (Epithelial Cell Adhesion Mol., also known as TACSTD1, encoded by gene GA733-2) are used as the major therapeutic targets (both sequences claimed but not provided). In addition, the invention provides methods for inhibiting metastasis in HCC patients by suppressing the function of one therapeutic target, osteopontin, and methods for preventing the development of HCC in patients with chronic liver diseases by suppressing the function of one therapeutic target, EpCAM. Pharmaceutical compns. containing agents capable of inhibiting the functions of osteopontin or EpCAM are also disclosed.

L10 ANSWER 3 OF 29 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 2003388610 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12925705
TITLE: **Centromere-associated protein -E** is essential for the mammalian mitotic checkpoint to prevent aneuploidy due to single chromosome loss.
AUTHOR: Weaver Beth A A; Bonday Zahid Q; Putkey Frances R; Kops Geert J P L; Silk Alain D; Cleveland Don W
CORPORATE SOURCE: Ludwig Institute for Cancer Research, 3080 CMM-East, 9500 Gilman Drive, La Jolla, CA 92093-0670, USA.
CONTRACT NUMBER: R37 GM 25913 (NIGMS)
T32 CA 67754 (NCI)
SOURCE: Journal of cell biology, (2003 Aug 18) 162 (4) 551-63. Journal code: 0375356. ISSN: 0021-9525.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200310
ENTRY DATE: Entered STN: 20030820
Last Updated on STN: 20031002
Entered Medline: 20031001

AB **Centromere-associated protein-E** (CENP-E) is an essential mitotic kinesin that is required for efficient, stable microtubule capture at kinetochores. It also directly binds to BubR1, a kinetochore-associated kinase implicated in the mitotic

checkpoint, the major cell cycle control pathway in which unattached kinetochores prevent anaphase onset. Here, we show that single unattached kinetochores depleted of CENP-E cannot block entry into anaphase, resulting in aneuploidy in 25% of divisions in primary mouse fibroblasts in vitro and in 95% of regenerating hepatocytes in vivo. Without CENP-E, diminished levels of BubR1 are recruited to kinetochores and BubR1 kinase activity remains at basal levels. CENP-E binds to and directly stimulates the kinase activity of purified BubR1 in vitro. Thus, CENP-E is required for enhancing recruitment of its binding partner BubR1 to each unattached kinetochore and for stimulating BubR1 kinase activity, implicating it as an essential amplifier of a basal mitotic checkpoint signal.

L10 ANSWER 4 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:72695 HCAPLUS
DOCUMENT NUMBER: 138:285029
TITLE: Melanoma Metastasis Suppression by Chromosome 6: Evidence for a Pathway Regulated by CRSP3 and TXNIP
AUTHOR(S): Goldberg, Steven F.; Miele, Mary E.; Hatta, Naohito; Takata, Minoru; Paquette-Straub, Carrie; Freedman, Leonard P.; Welch, Danny R.
CORPORATE SOURCE: Jake Gittlen Cancer Research Institute, Penn State College of Medicine, Hershey, PA, 17033, USA
SOURCE: Cancer Research (2003), 63(2), 432-440
CODEN: CNREA8; ISSN: 0008-5472
PUBLISHER: American Association for Cancer Research
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Loss of genetic material on chromosome 6 has been associated with progression of **human** melanomas. We showed previously that introducing chromosome 6 into metastatic **human** melanoma cell lines suppresses metastasis without affecting the ability of the hybrids to form progressively growing tumors. By subtractive hybridization comparing nonmetastatic chromosome 6-containing (neo6/C8161) vs. parental (C8161) metastatic cells, the KISS1 metastasis suppressor gene was isolated. However, KISS1 mapped to chromosome 1q32. To identify upstream regulator(s) of (and downstream effectors of) KISS1, microarray hybridization comparing C8161 and neo6/C8161 variants was performed. TXNIP/VDUP1, a thioredoxin-binding protein, was expressed more highly in neo6/C8161 and in nonmetastatic melanomas. Increased TXNIP expression inhibited metastasis and up-regulated KISS1. Surprisingly, TXNIP also mapped to chromosome 1q. PCR karyotyping that refined the region on chromosome 6 identified CRSP3/DRIP130, a transcriptional coactivator, as a metastasis suppressor. CRSP3 transfectant cells had up-regulated KISS1 and TXNIP expression and were suppressed for metastasis. Quant. real-time reverse-transcription PCR of clin. melanoma samples showed that loss of CRSP3 expression correlated with decreased KISS1 expression and increased metastasis. Thus, we implicated a specific gene on chromosome 6 in the etiol. of melanoma metastasis and identified potential up-stream regulators of KISS1 and TXNIP.
REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:731651 HCAPLUS
DOCUMENT NUMBER: 138:218703
TITLE: Role of Hec1 in Spindle Checkpoint Signaling and Kinetochore Recruitment of Mad1/Mad2
AUTHOR(S): Martin-Lluesma, Silvia; Stucke, Volker M.; Nigg, Erich A.
CORPORATE SOURCE: Department of Cell Biology, Max-Planck-Institute of Biochemistry, Martinsried, D-82152, Germany
SOURCE: Science (Washington, DC, United States) (2002), 297(5590), 2267-2270
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The spindle checkpoint delays sister chromatid separation until all chromosomes have undergone bipolar spindle attachment. Checkpoint failure may result in chromosome mis-segregation and may contribute to tumorigenesis. We showed that the **human** protein Hec1 was required for the recruitment of Mps1 kinase and Mad1/Mad2 complexes to kinetochores. Depletion of Hec1 impaired chromosome congression and caused persistent activation of the spindle checkpoint, indicating that high steady-state levels of Mad1/Mad2 complexes at kinetochores were not essential for checkpoint signaling. Simultaneous depletion of Hec1 and Mad2 caused catastrophic mitotic exit, making Hec1 an attractive target for the selective elimination of spindle checkpoint-deficient cells.
REFERENCE COUNT: 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 6 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:980229 HCAPLUS
DOCUMENT NUMBER: 138:351659
TITLE: Protein kinase TTK interacts and co-localizes with CENP-E to the kinetochore of **human** cells
AUTHOR(S): Zhang, Jie; Fu, Chuanhai; Miao, Yong; Dou, Zhen; Yao, Xuebiao
CORPORATE SOURCE: Laboratory of Cell Dynamics, University of Science & Technology of China, Hefei, 230027, Peop. Rep. China
SOURCE: Chinese Science Bulletin (2002), 47(23), 2005-2009
CODEN: CSBUEF; ISSN: 1001-6538
PUBLISHER: Science in China Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Spindle checkpoint is an important biochem. signaling cascade during mitosis which monitors the fidelity of chromosome segregation, and is mediated by protein kinases Mps1 and Bub1/BubR1. Our recent studies show that kinesin-related motor protein CENP-E interacts with BubR1 and participates in spindle checkpoint signaling. To elucidate the mol. mechanisms underlying spindle checkpoint signaling, we carried out proteomic dissection of **human** cell kinetochore and revealed protein kinase TTK, **human** homolog of yeast Mps1. Our studies show that TTK is localized to the kinetochore of **human** cells, and interacts with CENP-E, suggesting that TTK may play an important role in chromosome segregation during mitosis.
REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 7 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:770865 HCAPLUS
DOCUMENT NUMBER: 138:33911
TITLE: Generation of **human** artificial chromosomes expressing naturally controlled guanosine triphosphate cyclohydrolase I gene
AUTHOR(S): Ikeno, Masashi; Inagaki, Hidehito; Nagata, Keiko; Morita, Miwa; Ichinose, Hiroshi; Okazaki, Tuneko
CORPORATE SOURCE: Institute for Comprehensive Medical Science, Fujita Health University, Toyoake, 470-1192, Japan
SOURCE: Genes to Cells (2002), 7(10), 1021-1032
CODEN: GECEFL; ISSN: 1356-9597
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Human** artificial chromosomes (HACs) are generated from the precursor DNA constructs containing α-satellite DNA with CENP-B boxes, and the process could be used for the incorporation of large genes in the HACs. Guanosine triphosphate cyclohydrolase I (GCH1) is the first and

rate-limiting enzyme for the biosynthesis of tetrahydrobiopterin, the essential co-factor of aromatic amino acid hydroxylases and nitric oxide synthase. We constructed HACs carrying a 180 kb genome segment encoding the **human** GCH1 gene and its control region from the bacterial artificial chromosome (BAC) with the GCH1 segment by co-transfection with the α-satellite DNA-containing BAC to a **human** fibroblast cell line. Two cell lines carrying a HAC with GCH1 genes were obtained. Both HACs were composed of multiple copies of precursor BACs and were maintained stably in **human** and mouse cell lines. The GCH1 activities of the HAC-carrying **human** fibroblast cell lines were elevated but still highly sensitive to IFN-γ induction, mimicking the response of the gene expression from the authentic chromosomal genes. These HACs will provide a useful system for anal. of the complex regulatory circuit of the GCH1 gene in vivo and also function as a tool for gene delivery in animal models or in therapeutic trials.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 8 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:833805 HCAPLUS
DOCUMENT NUMBER: 138:268358
TITLE: Transient CENP-E-like kinetochore proteins in plants
AUTHOR(S): ten Hoopen, Rogier; Schleker, Thomas; Manteuffel, Renate; Schubert, Ingo
CORPORATE SOURCE: Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, 06466, Germany
SOURCE: Chromosome Research (2002), 10(7), 561-570
CODEN: CRRSEE; ISSN: 0967-3849
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Derived from candidate sequences of a barley EST database two proteins with homol. to the coiled coil region of the **human** kinetochore protein (KP) CENP-E were generated and classified as centromere protein E-like 1 and 2 (Cpel1 and Cpel2). Specific antibodies produced against recombinant Cpel1 and Cpel2 proteins labeled the centromere on mitotic chromosomes of barley and field bean and recognized specifically proteins from nuclear/chromosomal protein exts. on immunoblots. No function was predicted for homologs of Cpel1 within the databases for Arabidopsis and rice genomes. However, the centromeric location of Cpel1 and Cpel2 suggests they may have a function within the kinetochore. Plant homologs to barley Cpel2 are N-type kinesins, suggesting that Cpel2 is functionally homologous to **human** CENP-E.

REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 9 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2003:175910 BIOSIS
DOCUMENT NUMBER: PREV200300175910
TITLE: CENP-E is essential for the mammalian spindle assembly checkpoint to prevent single chromosome loss.
AUTHOR(S): Weaver, B. A. [Reprint Author]; Putkey, F. R. [Reprint Author]; Bonday, Z. Q. [Reprint Author]; Cleveland, D. W. [Reprint Author]
CORPORATE SOURCE: Cellular and Molecular Medicine, Ludwig Institute for Cancer Research and University of California, San Diego, La Jolla, CA, USA
SOURCE: Molecular Biology of the Cell, (Nov 2002) Vol. 13, No. Supplement, pp. 308a. print.
Meeting Info.: 42nd Annual Meeting of the American Society for Cell Biology. San Francisco, CA, USA. December 14-18, 2002. American Society for Cell Biology.
ISSN: 1059-1524 (ISSN print).
DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 9 Apr 2003
Last Updated on STN: 9 Apr 2003

L10 ANSWER 10 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:883090 HCAPLUS
DOCUMENT NUMBER: 138:399873
TITLE: Extensive cytogenetic analysis of a stable dicentric isochromosome 21, idic(21), formed by fusion of the terminal long arms
AUTHOR(S): Wandall, A.; Andersen, C.; Oestergaard, M.; Koch, Joern
CORPORATE SOURCE: Department of Medical Genetics, IMBG, Copenhagen, Den.
SOURCE: Cytogenetic and Genome Research (2002), 97(3-4), 145-148
CODEN: CGRYAJ; ISSN: 1424-8581
PUBLISHER: S. Karger AG
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The dicentric isochromosome 21 described in this paper was formed by fusion of the terminal parts of the long arms of two chromosomes 21. No interstitial telomeric AGGGTT repeats could be detected at the fusion point, but G-banding, comparative genomic hybridization, and fluorescence in situ hybridization with painting probes for 21qter revealed no loss of other terminal DNA sequences at the fusion point. Thus, only the telomeric repeats seem to have been lost prior to, or as a consequence of, isochromosome formation. Both short arms of the isochromosome were intact with complete NORs, and staining for α-satellite DNA showed that the DNA content of the two centromeres was the same. Antibody staining for the centromeric proteins CENP-C and CENP-E and for topoisomerase IIα and IIβ demonstrated that these proteins were localized predominantly or exclusively at the centromere in the primary constriction. A novel functional in situ assay for topoisomerase activity in vivo similarly demonstrated enzyme activity exclusively at the primary constriction centromere.
REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 11 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:52338 HCAPLUS
DOCUMENT NUMBER: 138:285274
TITLE: Genomic analysis of immediate/early response to shear stress in **human** coronary artery endothelial cells
AUTHOR(S): Peters, D. G.; Zhang, X.-C.; Benos, P. V.; Heidrich-O'Hare, E.; Ferrell, R. E.
CORPORATE SOURCE: Departments of Human Genetics, Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA, 15261, USA
SOURCE: Physiological Genomics (2002), 12(1), 25-33
CODEN: PHGEFP; ISSN: 1094-8341
URL: http://physiolgenomics.physiology.org/cgi/reprint/12/1/25.pdf
PUBLISHER: American Physiological Society
DOCUMENT TYPE: Journal; (online computer file)
LANGUAGE: English
AB The involvement of shear stress in the pathogenesis of vascular disease has motivated efforts to define the endothelial cell response to applied shear stress in vitro. A central question has been the mechanisms by which endothelial cells perceive and respond to changes in fluid flow. The authors have utilized cDNA microarrays to characterize the immediate/early genomic response to applied laminar shear stress (LSS) in primary cultures of **human** coronary artery endothelial cells

(HCAECs). Cells were exposed, in a parallel plate flow chamber, to 0, 15, or 45 dyn/cm2 LSS for 1 h, and gene expression profiles were determined using **human** GEM1 cDNA microarrays. The authors find that a high proportion of LSS-responsive genes are transcription factors, and these are related by their involvement in growth arrest. These likely play a central role in the reprogramming of endothelial homeostasis following the switch from a static to a shear-stressed environment. LSS-responsive genes were also found to encode factors involved in vasoreactivity, signal transduction, antioxidants, cell cycle-associated genes, and markers of cytoskeletal function and dynamics.

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 12 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:560807 HCAPLUS
DOCUMENT NUMBER: 135:238276
TITLE: Purification and characterization of native conventional kinesin, HSET, and CENP-E from mitotic HeLa cells
AUTHOR(S): DeLuca, Jennifer G.; Newton, Cori N.; Himes, Richard H.; Jordan, Mary Ann; Wilson, Leslie
CORPORATE SOURCE: Department of Molecular, Cellular, and Developmental Biology and the Materials Research Laboratory, University of California, Santa Barbara, CA, 93106, USA
SOURCE: Journal of Biological Chemistry (2001), 276(30), 28014-28021
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The authors have developed a strategy for the purification of native microtubule motor proteins from mitotic HeLa cells and describe here the purification and characterization of **human** conventional kinesin and two **human** kinesin-related proteins, HSET and CENP-E. The authors found that the 120-kDa HeLa cell conventional kinesin is an active motor that induces microtubule gliding at .apprx.30 μm/min at room temperature This active form of HeLa cell kinesin does not contain light chains, although light chains were detected in other fractions. HSET, a member of the C-terminal kinesin subfamily, was also purified in native form for the first time, and the protein migrates as a single band at .apprx.75 kDa. The purified HSET is an active motor that induces microtubule gliding at a rate of .apprx.5 μm/min, and microtubules glide for an average of 3 μm before ceasing movement. Finally, the authors purified native CENP-E, a kinesin-related protein that has been implicated in chromosome congression during mitosis, and the authors found that this form of CENP-E does not induce microtubule gliding but is able to bind to microtubules.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 13 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:800969 HCAPLUS
DOCUMENT NUMBER: 136:35329
TITLE: Specification of kinetochore-forming chromatin by the histone H3 variant CENP-A
AUTHOR(S): Van Hooser, Aaron A.; Ouspenski, Ilia I.; Gregson, Heather C.; Starr, Daniel A.; Yen, Tim J.; Goldberg, Michael L.; Yokomori, Kyoko; Earnshaw, William C.; Sullivan, Kevin F.; Brinkley, B. R.
CORPORATE SOURCE: Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, TX, 77030, USA
SOURCE: Journal of Cell Science (2001), 114(19), 3529-3542

CODEN: JNCSAI; ISSN: 0021-9533
PUBLISHER: Company of Biologists Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The mechanisms that specify precisely where mammalian kinetochores form within arrays of centromeric heterochromatin remain largely unknown. Localization of CENP-A exclusively beneath kinetochore plates suggests that this distinctive histone might direct kinetochore formation by altering the structure of heterochromatin within a sub-region of the centromere. To test this hypothesis, we exptl. mistargeted CENP-A to non-centromeric regions of chromatin and determined whether other centromere-kinetochore components were recruited. CENP-A-containing non-centromeric chromatin assembles a subset of centromere-kinetochore components, including CENP-C, hSMC1, and HZwint-1 by a mechanism that requires the unique CENP-A N-terminal tail. The sequence-specific DNA-binding protein CENP-B and the microtubule-associated proteins CENP-E and HZW10 were not recruited, and neocentromeric activity was not detected. Exptl. mistargeting of CENP-A to inactive centromeres or to acentric double-minute chromosomes was also not sufficient to assemble complete kinetochore activity. The recruitment of centromere-kinetochore proteins to chromatin appears to be a unique function of CENP-A, as the mistargeting of other components was not sufficient for assembly of the same complex. Our results indicate at least two distinct steps in kinetochore assembly: (1) precise targeting of CENP-A, which is sufficient to assemble components of a centromere-prekinetochore scaffold; and (2) targeting of kinetochore microtubule-associated proteins by an addnl. mechanism present only at active centromeres.
REFERENCE COUNT: 77 THERE ARE 77 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 14 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:524627 HCAPLUS
DOCUMENT NUMBER: 136:335799
TITLE: Cytogenetic analysis and construction of a BAC contig across a common neocentromeric region from 9p
AUTHOR(S): Satinover, D. L.; Vance, G. H.; Van Dyke, D. L.; Schwartz, S.
CORPORATE SOURCE: Department of Genetics and Center for Human Genetics, Case Western Reserve University School of Medicine and University Hospitals Cleveland, Cleveland, OH, 44106-9959, USA
SOURCE: Chromosoma (2001), 110(4), 275-283
CODEN: CHROAU; ISSN: 0009-5915
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Over 40 cases of neocentric marker chromosomes, without detectable α-satellite DNA, have been reported. Although these have originated from many different chromosomes, a few of these chromosomes have been involved in multiple cases of marker formation. In this study, two different markers originating from the short arm of chromosome 9 were analyzed, identifying a common neocentromeric region. A bacterial artificial chromosome (BAC) contig extending over more than 900 kb has been assembled across this neocentromeric region. Fluorescent in situ hybridization and immunofluorescence assays (CENP-C and CENP-E) have localized the neocentromere to a 500 kb region. Preliminary anal. of DNA sequences in this neocentromere revealed a highly AT-rich region, which also has an increase in the level of retroviral elements compared with the average levels in the genome.
REFERENCE COUNT: 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 15 OF 29 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2000494605 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10934468
TITLE: CENP-E forms a link between attachment of spindle microtubules to kinetochores and the mitotic checkpoint.
AUTHOR: Yao X; Abrieu A; Zheng Y; Sullivan K F; Cleveland D W
CORPORATE SOURCE: Department of Physiology, University of Wisconsin, Madison, Wisconsin 53706, USA.
CONTRACT NUMBER: GM29513 (NIGMS)
SOURCE: Nature cell biology, (2000 Aug) 2 (8) 484-91.
Journal code: 100890575. ISSN: 1465-7392.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001019

AB Here we show that suppression of synthesis of the microtubule motor CENP-E (**centromere-associated protein E**), a component of the kinetochore corona fibres of mammalian centromeres, yields chromosomes that are chronically mono-orientated, with spindles that are flattened along the plane of the substrate. Despite apparently normal microtubule numbers and the continued presence at kinetochores of other microtubule motors, spindle poles fragment in the absence of CENP-E, which implicates this protein in delivery of components from kinetochores to poles. CENP-E represents a link between attachment of spindle microtubules and the mitotic checkpoint signalling cascade, as depletion of this motor leads to profound checkpoint activation, whereas immunoprecipitation reveals a nearly stoichiometric association of CENP-E with the checkpoint kinase BubR1 during mitosis.

L10 ANSWER 16 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:375560 HCAPLUS
DOCUMENT NUMBER: 131:28641
TITLE: Genes encoding BUB proteins involved in mitotic checkpoint control and their use in design of anti-proliferative agents
INVENTOR(S): Yen, Timothy; Chan, Gordon; Jablonski, Sandra
PATENT ASSIGNEE(S): Fox Chase Cancer Center, USA
SOURCE: PCT Int. Appl., 99 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9928334	A1	19990610	WO 1998-US25415	19981201
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9916140	A1	19990616	AU 1999-16140	19981201
US 6593098	B1	20030715	US 2000-555554	20000601

PRIORITY APPLN. INFO.: US 1997-67093P P 19971201
WO 1998-US25415 W 19981201

AB Novel **human** BUB genes and their encoded proteins are provided herein. **Human** BUB1A is a protein kinase with a deduced mol. weight of 115-130 kDa, comprising a tripartite domain structure including an N-terminal kinetochore targeting domain, a central α-helical coil domain, and a C-terminal kinase domain. The protein demonstrates significant binding affinity for CENP-E, a kinesin-related protein which localizes to the kinetochore. **Human** BUB1B protein is 110-140 kDa and appears to be the **human** homolog of mouse BUB1. The

encoded protein is also a protein kinase and demonstrates significant binding affinity for CENP-F, a protein involved in the assembly and formation of a mature trilaminar kinetochore. **Human** BUB3 protein is 35-40 kDa in size and comprises five WD-40 motif repeats and complexes with **human** BUB1A. The BUB3 protein also localizes to the kinetochores during mitosis. The kinases encoded by the disclosed BUB1A and BUB1B genes play a pivotal role in mitotic checkpoint control. BUB3 is a substrate of these kinases. BUB genes and their encoded proteins provide valuable therapeutic targets for the design of anti-proliferative agents which inhibit the aberrant cellular proliferation observed in tumor cells.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 17 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:586035 HCAPLUS
DOCUMENT NUMBER: 131:298020
TITLE: **Human** BUBR1 is a mitotic checkpoint kinase that monitors CENP-E functions at kinetochores and binds the cyclosome/APC
AUTHOR(S): Chan, G. K. T.; Jablonski, S. A.; Sudakin, V.; Hittle, J. C.; Yen, T. J.
CORPORATE SOURCE: Fox Chase Cancer Center, Institute for Cancer Research, Philadelphia, PA, 19111, USA
SOURCE: Journal of Cell Biology (1999), 146(5), 941-954
CODEN: JCLBA3; ISSN: 0021-9525
PUBLISHER: Rockefeller University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Human** cells express two kinases that are related to the yeast mitotic checkpoint kinase BUB1. HBUB1 and hBUBR1 bind to kinetochores where they are postulated to be components of the mitotic checkpoint that monitors kinetochore activities to determine if chromosomes have achieved alignment at the spindle equator. In support of this, hBUB1 and the homologous mouse BUB1 have been shown to be important for the mitotic checkpoint. We now demonstrate that hBUBR1 is also an essential component of the mitotic checkpoint. HBUBR1 is required by cells that are exposed to microtubule inhibitors to arrest in mitosis. Addnl., hBUBR1 is essential for normal mitotic progression as it prevents cells from prematurely entering anaphase. We establish that one of hBUBR1's checkpoint functions is to monitor kinetochore activities that depend on the kinetochore motor CENP-E. HBUBR1 is expressed throughout the cell cycle, but its kinase activity is detected after cells have entered mitosis. HBUBR1 kinase activity was rapidly stimulated when the spindle was disrupted in mitotic cells. Finally, hBUBR1 was associated with the cyclosome/anaphase-promoting complex (APC) in mitotically arrested cells but not in interphase cells. The combined data indicate that hBUBR1 can potentially provide two checkpoint functions by monitoring CENP-E-dependent activities at the kinetochore and regulating cyclosome/APC activity.

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 18 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1999:287981 BIOSIS
DOCUMENT NUMBER: PREV199900287981
TITLE: CENP-E interacts with BubR1 and participates in spindle assembly checkpoint signaling in **human** gastric carcinoma cells.
AUTHOR(S): Yao, Xuebiao [Reprint author]; Zheng, Y.
CORPORATE SOURCE: Univ of Wisconsin, Madison, WI, USA
SOURCE: Gastroenterology, (April, 1999) Vol. 116, No. 4 PART 2, pp. A533. print.
Meeting Info.: Digestive Disease Week and the 100th Annual

Meeting of the American Gastroenterological Association. Orlando, Florida, USA. May 16-19, 1999. American Gastroenterological Association.
CODEN: GASTAB. ISSN: 0016-5085.

DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Aug 1999
Last Updated on STN: 5 Aug 1999

L10 ANSWER 19 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:640363 HCAPLUS
DOCUMENT NUMBER: 129:258972
TITLE: Identification of tumor-associated alleles of genes essential for cell viability and growth and the development of neoplasm inhibitors targeted against them
INVENTOR(S): Housman, David; Ledley, Fred D.; Stanton, Vincent P., Jr.
PATENT ASSIGNEE(S): Variagenics, Inc., USA
SOURCE: PCT Int. Appl., 605 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9841648	A2	19980924	WO 1998-US5419	19980319
WO 9841648	A3	19990429		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9867643	A1	19981012	AU 1998-67643	19980319
EP 973935	A2	20000126	EP 1998-912974	19980319
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1997-41057P P 19970320
WO 1998-US5419 W 19980319

AB Strategies for the identification and targeting of specific alleles of genes in the treatment of tumors are described. Tumor-associated alleles of genes coding for proteins essential for cell viability or cell growth and that show loss of an alleles in cancer cells due to loss of heterozygosity (LOH) are identified. Inhibitors of the remaining allele, such as antisense nucleic acids or ribozymes, can then be developed. The method can also be used to inhibit the expression of particular alleles of genes for antigens in the control of transplant rejection. Particular categories of appropriate target genes are described, along with specific exemplary genes within those categories and methods of using such target genes. Antisense phosphorothioate oligonucleotides targeting RNA polymerase II and glutamyl/prolyl tRNA synthetase genes were tested for cytotoxicity in vitro. Oligonucleotides with a single base mismatch were significantly less toxic than those without mismatches. A number of genes essential for proliferation were mapped and shown to be affected by loss-of-heterozygosity in oncogenesis.

L10 ANSWER 20 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:43173 HCAPLUS
DOCUMENT NUMBER: 131:41026
TITLE: The hBUB1 and hBUBR1 kinases sequentially assemble

onto kinetochores during prophase with hBUBR1 concentrating at the kinetochore plates in mitosis

AUTHOR(S): Jablonski, S. A.; Chan, G. K. T.; Cooke, C. A.; Earnshaw, W. C.; Yen, T. J.

CORPORATE SOURCE: Fox Chase Cancer Center, Philadelphia, PA, 19111, USA

SOURCE: Chromosoma (1998), 107(6-7), 386-396
CODEN: CHROAU; ISSN: 0009-5915

PUBLISHER: Springer-Verlag

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The kinetochore binds an evolutionarily conserved set of checkpoint proteins that function to monitor whether chromosomes have aligned properly at the spindle equator. **Human** cells contain two related protein kinases, hBUB1 and hBUBR1, that appear to have evolved from a single ancestral BUB1 gene. We generated hBUB1- and hBUBR1-specific antibodies so that the localization patterns of these kinases could be directly compared. In the **human** U2OS osteosarcoma cell line, hBUB1 first appeared at kinetochores during early prophase before all kinetochores were occupied by hBUBR1 or CENP-F. Both proteins remained at kinetochores throughout mitosis but their staining intensity was reduced from anaphase onward. Kinetochores of unaligned chromosomes exhibited stronger hBUB1 and hBUBR1 staining. Immunoelectron microscopy showed that hBUBR1 appeared to be concentrated in the outer kinetochore plate and in some instances the inner plate as well. When chromosome spreads were examined by light microscopy, hBUB1 and hBUBR1 were coincident with CENP-E. This suggests that both kinases are concentrated near the surface of the kinetochore where they can monitor kinetochore-microtubule interactions.

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:500471 HCAPLUS

DOCUMENT NUMBER: 127:200824

TITLE: Characterization of neo-centromeres in marker chromosomes lacking detectable alpha-satellite DNA

AUTHOR(S): Depinet, Theresa W.; Zackowski, Joleen L.; Earnshaw, William C.; Kaffe, Sara; Sekhon, Gurbax S.; Stallard, Richard; Sullivan, Beth A.; Vance, Gail H.; Van Dyke, Daniel L.; Willard, Huntington F.; Zinn, Arthur B.; Schwartz, Stuart

CORPORATE SOURCE: Department Genetics, Center Human Genetics, Case Western Reserve University School Medicine and University Hospitals of Cleveland, Cleveland, OH, 44106-9959, USA

SOURCE: Human Molecular Genetics (1997), 6(8), 1195-1204
CODEN: HMGEE5; ISSN: 0964-6906

PUBLISHER: Oxford University Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Recent studies have implicated α-satellite DNA as an integral part of the centromere, important for the normal segregation of **human** chromosomes. To explore the relationship between the normal functioning centromere and α-satellite DNA, 8 accessory marker chromosomes were studied in which fluorescence in-situ hybridization could detect neither pancentromeric nor chromosome-specific α-satellite DNA. These accessory marker chromosomes were present in the majority of or all cells analyzed and appeared mitotically stable, thereby indicating the presence of a functional centromere. FISH anal. with both chromosome-specific libraries and single-copy YACs, together with microsatellite DNA studies, allowed unequivocal identification of both the origin and structure of these chromosomes. All but one of the marker chromosomes were linear mirror image duplications, and they were present along with either 2 addnl. normal chromosomes or with 1 normal and 1 deleted chromosome.

Indirect immunofluorescence anal. revealed that the centromere protein CENP-B was not present on these markers; both CENP-C and CENP-E were present at a position defining a 'neo-centromere'. These studies provide insight into a newly defined class of marker chromosomes that lack detectable α-satellite DNA. At least for such marker chromosomes, α-satellite DNA at levels detectable by FISH appears unnecessary for chromosome segregation or for the association of CENP-C and CENP-E at a functional centromere.

L10 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:770764 HCAPLUS
DOCUMENT NUMBER: 128:178653
TITLE: Localization of CENP-E in the fibrous corona and outer plate of mammalian kinetochores from prometaphase through anaphase
AUTHOR(S): Cooke, Carol A.; Schaar, Bruce; Yen, Tim J.; Earnshaw, William C.
CORPORATE SOURCE: King's Buildings, Michael Swann Building, Institute of Cell and Molecular Biology, University of Edinburgh, Mayfield Road, Edinburgh, EH9 3JR, UK
SOURCE: Chromosoma (1997), 106(7), 446-455
CODEN: CHROAU; ISSN: 0009-5915
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have conducted a detailed ultrastructural anal. of the distribution of the kinesin-related centromere protein CENP-E during mitosis in cultured **human**, rat kangaroo and Indian muntjac cells. Using an affinity-purified polyclonal antibody and detection by 0.8 nm colloidal gold particles, CENP-E was localized primarily to the fibrous corona of the kinetochore in prometaphase and metaphase cells. Some labeling of the kinetochore outer plate was also observed The distribution of fibrous corona-associated CENP-E did not change dramatically following the attachment of microtubules to the kinetochore. Thus, the normal disappearance of this kinetochore substructure in conventional electron micrographs of mitotic chromosomes with attached kinetochores is not due to the corona becoming stretched along the spindle microtubules as has been suggested. Examination of cells undergoing anaphase chromatid movement revealed the presence of CENP-E still associated with the outer surface of the kinetochore plate. At the same time, the majority of detectable CENP-E in these cells was associated with the bundles of antiparallel microtubules in the central spindle. CENP-E in this region of the cell is apparently associated with the stem body matrix material. The simultaneous localization of CENP-E on centromeres and the central spindle during anaphase was confirmed by both wide-field microscopy of **human** cells and conventional fluorescence microscopy of rat kangaroo cells. Together, the observations reported here are consistent with models in which CENP-E has a role in promoting the poleward migration of sister chromatids during anaphase A.
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 23 OF 29 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 97477390 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9334346
TITLE: The microtubule-dependent motor **centromere-associated protein E** (CENP-E) is an integral component of kinetochore corona fibers that link centromeres to spindle microtubules.
AUTHOR: Yao X; Anderson K L; Cleveland D W
CORPORATE SOURCE: Laboratory of Cell Biology, Ludwig Institute for Cancer Research, School of Medicine, University of California, La Jolla, CA 92093-0660, USA.
CONTRACT NUMBER: GM 29513 (NIGMS)
SOURCE: Journal of cell biology, (1997 Oct 20) 139 (2) 435-47.

Journal code: 0375356. ISSN: 0021-9525.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199711
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971120

AB **Centromere-associated protein E** (CENP-E) is a kinesin-related microtubule motor protein that is essential for chromosome congression during mitosis. Using immunoelectron microscopy, CENP-E is shown to be an integral component of the kinetochore corona fibers that tether centromeres to the spindle. Immediately upon nuclear envelope fragmentation, an associated plus end motor trafficks cytoplasmic CENP-E toward chromosomes along astral microtubules that enter the nuclear volume. Before or concurrently with initial lateral attachment of spindle microtubules, CENP-E targets to the outermost region of the developing kinetochores. After stable attachment, throughout chromosome congression, at metaphase, and throughout anaphase A, CENP-E is a constituent of the corona fibers, extending at least 50 nm away from the kinetochore outer plate and intertwining with spindle microtubules. In congressing chromosomes, CENP-E is preferentially associated with (or accessible at) the stretched, leading kinetochore known to provide the primary power for chromosome movement. Taken together, this evidence strongly supports a model in which CENP-E functions in congression to tether kinetochores to the disassembling microtubule plus ends.

L10 ANSWER 24 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1996:53950 BIOSIS
DOCUMENT NUMBER: PREV199698626085
TITLE: The identification and cloning of a novel cell cycle specific centromere protein.
AUTHOR(S): Mack, G.; Fritzler, M. J.; Rattner, J. B.
CORPORATE SOURCE: Dep. Med. Biochem., Univ. Calgary, Calgary, AB, Canada
SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. SUPPL., pp. 362A.
Meeting Info.: Thirty-fifth Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 9-13, 1995.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Feb 1996
Last Updated on STN: 2 Feb 1996

L10 ANSWER 25 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1996:53947 BIOSIS
DOCUMENT NUMBER: PREV199698626082
TITLE: CENP-E organization at kinetochores is modulated by spindle microtubule attachment.
AUTHOR(S): Thrower, D. A.; Jordan, M. A.; Wilson, L.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Calif., Santa Barbara, CA 93106, USA
SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. SUPPL., pp. 361A.
Meeting Info.: Thirty-fifth Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 9-13, 1995.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)

LANGUAGE: English
ENTRY DATE: Entered STN: 2 Feb 1996
Last Updated on STN: 2 Feb 1996

L10 ANSWER 26 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1996:53949 BIOSIS
DOCUMENT NUMBER: PREV199698626084
TITLE: CENP-E is kinetochore-associated throughout anaphase.
AUTHOR(S): Brown, K. D. [Reprint author]; Wood, K. W.; Schroer, T. A.; Cleveland, D. W. [Reprint author]
CORPORATE SOURCE: Dep. Biol. Chem., Johns Hopkins Sch. Med., Baltimore, MD, USA
SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. SUPPL., pp. 361A.
Meeting Info.: Thirty-fifth Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 9-13, 1995.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Feb 1996
Last Updated on STN: 2 Feb 1996

L10 ANSWER 27 OF 29 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1996:53945 BIOSIS
DOCUMENT NUMBER: PREV199698626080
TITLE: Molecular analysis of CENP-E: Identification of the kinetochore localization domain.
AUTHOR(S): Chan, Gordon K. T.; Wu, Ginger; Yen, Tim
CORPORATE SOURCE: Fox Chase Cancer Cent., Philadelphia, PA 19111, USA
SOURCE: Molecular Biology of the Cell, (1995) Vol. 6, No. SUPPL., pp. 361A.
Meeting Info.: Thirty-fifth Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 9-13, 1995.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Feb 1996
Last Updated on STN: 2 Feb 1996

L10 ANSWER 28 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1995:191550 HCAPLUS
DOCUMENT NUMBER: 122:206533
TITLE: Chromosomal localization of the genes encoding the kinetochrome proteins CENPE and CENPF to **human** chromosomes 4q24 → q25 and 1q32 → q41, respectively, by fluorescence in situ hybridization
AUTHOR(S): Testa, Joseph R.; Zhou, Jian-Yuan; Bell, Daphne W.; Yen, Tim J.
CORPORATE SOURCE: Department of Medical Oncology, Fox Chase Cancer Center, Philadelphia, PA, 19111, USA
SOURCE: Genomics (1994), 23(3), 691-3
CODEN: GNMCEP; ISSN: 0888-7543
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
AB CENPE and CENPF are **human** kinetochore proteins of 312 and .apprx.400 kDa, resp. As part of an effort to characterize the functions of these 2 proteins, the authors have used their resp. cDNAs to map their

human chromosomal locations by fluorescence in situ hybridization. The gene that encodes CENPE, a kinetochore-associated motor protein that is postulated to segregate chromosomes during mitosis, maps to chromosome 4q24 → q25. The CENPF gene, which encodes a structural protein of the kinetochore, maps to chromosome 1q32 → q41 within close proximity to the genetic locus that is linked to Van der Woude syndrome.

L10 ANSWER 29 OF 29 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:511514 HCAPLUS
DOCUMENT NUMBER: 119:111514
TITLE: CENP-E is a putative kinetochore motor that accumulates just before mitosis
AUTHOR(S): Yen, Tim J.; Li, Gang; Schaar, Bruce T.; Szilak, Illya; Cleveland, Don W.
CORPORATE SOURCE: Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA
SOURCE: Nature (London, United Kingdom) (1992), 359(6395), 536-9
CODEN: NATUAS; ISSN: 0028-0836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB CENP-E is identified as a kinesin-like motor protein (Mr 312,000) that accumulates in the G2 phase of the cell cycle. CENP-E assocs. with kinetochores during congression, relocates to the spindle midzone at anaphase, and is quant. discarded at the end of the cell division. CENP-E is likely to be one of the motors responsible for mammalian chromosome movement and/or spindle elongation.

=> d his

(FILE 'HOME' ENTERED AT 14:59:52 ON 26 MAR 2004)

FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS, LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004

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L1         13661 S KINESIN
L2          2217 S HUMAN AND L1
L3          3637 S "MOTOR DOMAIN?"
L4           328 S L2 AND L3
L5           777 S "CENP-E"
L6            12 S L4 AND L5
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)
L8            74 S "CENTROMERE-ASSOCIATED PROTEIN-E"
L9            34 S HUMAN AND L8
L10           29 DUP REM L9 (5 DUPLICATES REMOVED)

=> s "unglycosylat"
L11            0 "UNGLYCOSYLAT"

=> s unglycosylaed"
MISMATCHED QUOTE 'LYCOSYLAED"'
Quotation marks (or apostrophes) must be used in pairs,
one before and one after the expression you are setting
off or masking.

=> s unglycosylated"
MISMATCHED QUOTE 'YCOSYLATED"'
Quotation marks (or apostrophes) must be used in pairs,
one before and one after the expression you are setting
off or masking.

=> s unglycosylated
L12         4821 UNGLYCOSYLATED

=> s l10 or l5
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L13 778 L10 OR L5

=> s l12 and l13
L14 1 L12 AND L13

=> d all

L14 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2004 ACS on STN
AN 2000:756837 HCAPLUS
DN 133:318271
ED Entered STN: 27 Oct 2000
TI Recombinant bacterial expression and purification of human kinesins
IN Beraud, Christophe; Ohashi, Cara; Sakowicz, Roman; Wood, Ken; Vaisberg, Eugeni; Yu, Ming
PA Cytokinetics, USA
SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N009-16
ICS C12N015-00; C12N001-20
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 9, 10, 13, 16
FAN.CNT 5

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000063353	A1	20001026	WO 2000-US10870	20000420
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6544766	B1	20030408	US 2000-595684	20000616
	US 6387644	B1	20020514	US 2000-724224	20001128
	US 2003044900	A1	20030306	US 2001-45631	20011019
PRAI	US 1999-295612	A1	19990420		
	WO 2000-US10870	A1	20000420		
	US 2000-597292	B1	20000620		

AB Described herein are methods of producing kinesins. In a preferred embodiment, the kinesins are produced from a prokaryote, most preferably, a bacterial cell. Bacterial expression offers several advantages over systems previously utilized, such as, for example, Baculovirus. The yield of protein is higher, the cost of the expression setup is lower, and creation of alternative expression vectors is easier. The concern of copurifying a contaminating activity from the expression host is also eliminated since bacteria, in contrast to the baculovirus expression system, do not have kinesin-like proteins. Also described herein are purified kinesins, preferably **unglycosylated** and methods of use.

ST kinesin human cloning expression purifn
IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(ATSV; recombinant bacterial expression and purification of human kinesins)
IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**CENP-E**; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(HSET; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(KSP; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Kid; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(Kin2; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(MCAK; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(MKLP1; recombinant bacterial expression and purification of human kinesins)

IT Microtubule
(assay for binding activity of; recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(chromokinesin; recombinant bacterial expression and purification of human kinesins)

IT Bacteria (Eubacteria)
Drug screening
Molecular cloning
(recombinant bacterial expression and purification of human kinesins)

IT Kinesins
RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(recombinant bacterial expression and purification of human kinesins)

IT Epitopes
(tags; recombinant bacterial expression and purification of human kinesins)

IT 302995-11-5 302995-12-6 302995-13-7 302995-14-8 302995-15-9
302995-16-0 302995-17-1 302995-18-2 302995-19-3 302995-20-6
302995-21-7 302995-22-8 302995-23-9 302995-24-0 302995-25-1
302995-26-2 302995-27-3 302995-28-4 302995-29-5 302995-30-8
302995-31-9 302995-33-1 302995-34-2 302995-35-3 302995-36-4
302995-37-5 302995-38-6 302995-39-7 302995-40-0 302995-41-1
302995-42-2 302995-43-3 302995-44-4 302995-45-5 302995-46-6
302995-47-7 302995-48-8 302995-49-9 302995-50-2 302995-51-3
302995-52-4 302995-53-5 302995-54-6 302995-55-7 302995-56-8
302995-57-9 302995-58-0 302995-59-1 302995-60-4 302995-61-5
302995-62-6 302995-63-7 302995-64-8 302995-65-9 302995-66-0
302995-67-1 302995-68-2 302995-69-3 302995-70-6 302995-71-7
302995-72-8 302995-73-9 302995-74-0 302995-75-1
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES

```
     (Uses)
        (PCR primer for kinesin cDNA cloning; recombinant bacterial expression
        and purification of human kinesins)
IT   302995-32-0
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (PCR primer for myc epitope tag; recombinant bacterial expression and
        purification of human kinesins)
IT   190858-49-2P, Kinesin-2 (human gene HK2)   301803-60-1P,
     2-335-Chromokinesin (human)   301803-61-2P, 2-475-Chromokinesin (human)
     301803-62-3P, 2-679-Chromokinesin (human)   301803-63-4P,
     2-1231-Chromokinesin (human)   301803-64-5P, 166-532-Kinesin 2 (human gene
     HK2)   301803-65-6P, 195-532-Kinesin 2 (human gene HK2)   301803-66-7P
     301803-67-8P   301803-68-9P   301803-69-0P   301803-70-3P   301803-71-4P
     301803-72-5P   301803-73-6P   301803-74-7P   301803-75-8P   301803-76-9P
     301803-77-0P   301803-78-1P   301803-79-2P   301803-80-5P   301803-81-6P
     301803-82-7P   301803-83-8P   301803-84-9P   301803-85-0P   301803-86-1P
     301803-87-2P   301803-88-3P   301803-89-4P   301803-90-7P
     RL: BPN (Biosynthetic preparation); PRP (Properties); PUR (Purification or
     recovery); THU (Therapeutic use); BIOL (Biological study); PREP
     (Preparation); USES (Uses)
        (amino acid sequence; recombinant bacterial expression and purification of
        human kinesins)
IT   9000-83-3, ATpase
     RL: ANT (Analyte); ANST (Analytical study)
        (assay for activity of; recombinant bacterial expression and purification of
        human kinesins)
IT   145677-16-3, GenBank X67155   148087-13-2, GenBank Z15005   153518-24-2,
     GenBank D14678   172444-49-4, GenBank U37426   174058-47-0, GenBank X90840
     183845-82-1, GenBank U63743   188226-27-9, GenBank Y08319   216123-79-4,
     GenBank AB017430   224936-85-0, GenBank AF071592
     RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological
     study); USES (Uses)
        (nucleotide sequence; recombinant bacterial expression and purification of
        human kinesins)
RE.CNT  3     THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Wang; Chromokinesin:a DNA-binding, Kinesin-like Nuclear Protein 1995,
    V128(5), P761 HCAPLUS
(2) Wood; CENP-E Is a Plus End-Directed Kinetochore Motor Required for
    Metaphase Chromosome Alignment 1997, V91, P357 HCAPLUS
(3) Yen; CENP-E is a Putative Kinetochore Motor that Accumultes just before
    Mitosis 1992, V359, P536 HCAPLUS


=> e beraud c/au
E1            1     BERAUD ALEXANDRE/AU
E2            9     BERAUD B/AU
E3          473 --> BERAUD C/AU
E4            1     BERAUD C L/AU
E5            9     BERAUD CASSEL A M/AU
E6            2     BERAUD CATHERINE/AU
E7            1     BERAUD CEDRIC FRANCIS/AU
E8            1     BERAUD CH J/AU
E9          114     BERAUD CHRISTOPHE/AU
E10           4     BERAUD CL/AU
E11          17     BERAUD COLOMB E/AU
E12           1     BERAUD COLOMB ELIAINE/AU

=> s e3
L15         473 "BERAUD C"/AU

=> e ohashi c/au
E1            1     OHASHI B/AU
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E2            1      OHASHI B H/AU
E3           24 --> OHASHI C/AU
E4           15      OHASHI C T/AU
E5            8      OHASHI CARA/AU
E6            7      OHASHI CARA T/AU
E7            1      OHASHI CHE/AU
E8            1      OHASHI CHIAKI/AU
E9            3      OHASHI CHIE/AU
E10           1      OHASHI CHIGEO/AU
E11           1      OHASHI CHIGIRU/AU
E12           6      OHASHI CHIHIRO/AU

=> s e3-e7
L16          55 ("OHASHI C"/AU OR "OHASHI C T"/AU OR "OHASHI CARA"/AU OR "OHASHI
                CARA T"/AU OR "OHASHI CHE"/AU)

=> e sakowicz r/au
E1            1      SAKOWICZ MAREK/AU
E2           16      SAKOWICZ MONIKA/AU
E3           65 --> SAKOWICZ R/AU
E4            2      SAKOWICZ ROBERT/AU
E5           68      SAKOWICZ ROMAN/AU
E6            2      SAKOWICZ S/AU
E7           30      SAKOWICZ T/AU
E8           18      SAKOWICZ TOMASZ/AU
E9            1      SAKOWITSC/AU
E10           1      SAKOWITSCH K/AU
E11           1      SAKOWITSCH M/AU
E12           1      SAKOWITSCH W/AU

=> s e5
L17          68 "SAKOWICZ ROMAN"/AU

=> e vaisberg e/au
E1            3      VAISBERG CHAIKA/AU
E2            1      VAISBERG D/AU
E3           27 --> VAISBERG E/AU
E4           49      VAISBERG E A/AU
E5            3      VAISBERG E F/AU
E6            5      VAISBERG E I/AU
E7           23      VAISBERG E S/AU
E8            9      VAISBERG E V/AU
E9           14      VAISBERG ELENA/AU
E10           2      VAISBERG ELENA V/AU
E11           4      VAISBERG EUGENI/AU
E12          15      VAISBERG EUGENI A/AU

=> s e12
L18          15 "VAISBERG EUGENI A"/AU

=> e wood k/au
E1            1      WOOD JUSTIN A/AU
E2            2      WOOD JUSTIN G/AU
E3          781 --> WOOD K/AU
E4          190      WOOD K A/AU
E5           84      WOOD K B/AU
E6           39      WOOD K C/AU
E7           20      WOOD K D/AU
E8           85      WOOD K E/AU
E9           23      WOOD K F/AU
E10          25      WOOD K G/AU
E11          20      WOOD K H/AU
E12           2      WOOD K H B/AU
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=> s e3
L19         781 "WOOD K"/AU

=> e yu m/au
E1            1     YU LYNN K/AU
E2            1     YU LYU/AU
E3         2239 --> YU M/AU
E4            1     YU M */AU
E5           22     YU M A/AU
E6           75     YU M B/AU
E7          931     YU M C/AU
E8           12     YU M C Z/AU
E9            2     YU M CHRISTINA/AU
E10          29     YU M D/AU
E11           8     YU M E/AU
E12           1     YU M ELISA/AU

=> s e3
L20        2239 "YU M"/AU

=> d his

     (FILE 'HOME' ENTERED AT 14:59:52 ON 26 MAR 2004)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004
L1         13661 S KINESIN
L2          2217 S HUMAN AND L1
L3          3637 S "MOTOR DOMAIN?"
L4           328 S L2 AND L3
L5           777 S "CENP-E"
L6            12 S L4 AND L5
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)
L8            74 S "CENTROMERE-ASSOCIATED PROTEIN-E"
L9            34 S HUMAN AND L8
L10           29 DUP REM L9 (5 DUPLICATES REMOVED)
L11            0 S "UNGLYCOSYLAT"
L12         4821 S UNGLYCOSYLATED
L13          778 S L10 OR L5
L14            1 S L12 AND L13
                 E BERAUD C/AU
L15          473 S E3
                 E OHASHI C/AU
L16           55 S E3-E7
                 E SAKOWICZ R/AU
L17           68 S E5
                 E VAISBERG E/AU
L18           15 S E12
                 E WOOD K/AU
L19          781 S E3
                 E YU M/AU
L20         2239 S E3

=> e beraud c
E1            2     BERAUCKSICHTIGUNG/BI
E2           15     BERAUD/BI
E3            0 --> BERAUD C/BI
E4            9     BERAUDI/BI
E5            1     BERAUDIERE/BI
E6            2     BERAUH/BI
E7            2     BERAULT/BI
E8            1     BERAUMUNG/BI
E9            4     BERAUN/BI
E10           2     BERAUNIA/BI
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E11          60      BERAUNITE/BI
E12           3      BERAUSCHENDE/BI

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E1            1      BERAUD ALEXANDRE/AU
E2            9      BERAUD B/AU
E3          473 --> BERAUD C/AU
E4            1      BERAUD C L/AU
E5            9      BERAUD CASSEL A M/AU
E6            2      BERAUD CATHERINE/AU
E7            1      BERAUD CEDRIC FRANCIS/AU
E8            1      BERAUD CH J/AU
E9          114      BERAUD CHRISTOPHE/AU
E10           4      BERAUD CL/AU
E11          17      BERAUD COLOMB E/AU
E12           1      BERAUD COLOMB ELIAINE/AU

=> s e9
L21         114 "BERAUD CHRISTOPHE"/AU

=> d his

     (FILE 'HOME' ENTERED AT 14:59:52 ON 26 MAR 2004)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004
L1         13661 S KINESIN
L2          2217 S HUMAN AND L1
L3          3637 S "MOTOR DOMAIN?"
L4           328 S L2 AND L3
L5           777 S "CENP-E"
L6            12 S L4 AND L5
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)
L8            74 S "CENTROMERE-ASSOCIATED PROTEIN-E"
L9            34 S HUMAN AND L8
L10           29 DUP REM L9 (5 DUPLICATES REMOVED)
L11            0 S "UNGLYCOSYLAT"
L12         4821 S UNGLYCOSYLATED
L13          778 S L10 OR L5
L14            1 S L12 AND L13
                 E BERAUD C/AU
L15          473 S E3
                 E OHASHI C/AU
L16           55 S E3-E7
                 E SAKOWICZ R/AU
L17           68 S E5
                 E VAISBERG E/AU
L18           15 S E12
                 E WOOD K/AU
L19          781 S E3
                 E YU M/AU
L20         2239 S E3
                 E BERAUD C
                 E BERAUD C/AU
L21          114 S E9

=> e l16 or l17 or l18 or l19 or l20 or l21
E1            1      L15XT1/BI
E2         1503      L16/BI
E3            0 --> L16 OR L17 OR L18 OR L19 OR L20 OR L21/BI
E4            1      L16.74/BI
E5           14      L160/BI
E6            6      L1600/BI
E7            1      L16003/BI
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E8            1     L1601/BI
E9            3     L16012/BI
E10           3     L16014/BI
E11           8     L16015/BI
E12          41     L16016/BI

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     (FILE 'HOME' ENTERED AT 14:59:52 ON 26 MAR 2004)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:00:14 ON 26 MAR 2004
L1         13661 S KINESIN
L2          2217 S HUMAN AND L1
L3          3637 S "MOTOR DOMAIN?"
L4           328 S L2 AND L3
L5           777 S "CENP-E"
L6            12 S L4 AND L5
L7             5 DUP REM L6 (7 DUPLICATES REMOVED)
L8            74 S "CENTROMERE-ASSOCIATED PROTEIN-E"
L9            34 S HUMAN AND L8
L10           29 DUP REM L9 (5 DUPLICATES REMOVED)
L11            0 S "UNGLYCOSYLAT"
L12         4821 S UNGLYCOSYLATED
L13          778 S L10 OR L5
L14            1 S L12 AND L13
                 E BERAUD C/AU
L15          473 S E3
                 E OHASHI C/AU
L16           55 S E3-E7
                 E SAKOWICZ R/AU
L17           68 S E5
                 E VAISBERG E/AU
L18           15 S E12
                 E WOOD K/AU
L19          781 S E3
                 E YU M/AU
L20         2239 S E3
                 E BERAUD C
                 E BERAUD C/AU
L21          114 S E9
                 E L2 OR L3

=> s l16 or l17 or l18 or l19 or l20 or l21
L22         3237 L16 OR L17 OR L18 OR L19 OR L20 OR L21

=> s l13 and l22
L23            6 L13 AND L22

=> dup rem l23
PROCESSING COMPLETED FOR L23
L24            5 DUP REM L23 (1 DUPLICATE REMOVED)

=> d 1-5 ibib ab

L24  ANSWER 1 OF 5  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER:   2004:7637  BIOSIS
DOCUMENT NUMBER:    PREV200400008401
TITLE:              Plus end-directed microtubule motor required for chromosome
                    congression.
AUTHOR(S):          Wood, Kenneth W. [Inventor, Reprint Author]; Sakowicz,
                    Roman [Inventor]; Goldstein, Lawrence S. B.
                    [Inventor]; Cleveland, Don W. [Inventor]
CORPORATE SOURCE:   Delmar, CA, USA
```

ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6645748 November 11, 2003
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov 11 2003) Vol. 1276, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 17 Dec 2003
Last Updated on STN: 17 Dec 2003

AB The invention provides isolated nucleic acid and amino acid sequences of Xenopus **CENP-E** (XCENP-E), antibodies to XCENP-E, methods of screening for **CENP-E** modulators using biologically active **CENP-E**, and kits for screening for **CENP-E** modulators.

L24 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:756837 HCAPLUS
DOCUMENT NUMBER: 133:318271
TITLE: Recombinant bacterial expression and purification of human kinesins
INVENTOR(S): **Beraud, Christophe**; **Ohashi, Cara**; **Sakowicz, Roman**; Wood, Ken; Vaisberg, Eugeni; Yu, Ming
PATENT ASSIGNEE(S): Cytokinetics, USA
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000063353	A1	20001026	WO 2000-US10870	20000420
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6544766	B1	20030408	US 2000-595684	20000616
US 6387644	B1	20020514	US 2000-724224	20001128
US 2003044900	A1	20030306	US 2001-45631	20011019

PRIORITY APPLN. INFO.: US 1999-295612 A1 19990420
WO 2000-US10870 A1 20000420
US 2000-597292 B1 20000620

AB Described herein are methods of producing kinesins. In a preferred embodiment, the kinesins are produced from a prokaryote, most preferably, a bacterial cell. Bacterial expression offers several advantages over systems previously utilized, such as, for example, Baculovirus. The yield of protein is higher, the cost of the expression setup is lower, and creation of alternative expression vectors is easier. The concern of copurifying a contaminating activity from the expression host is also eliminated since bacteria, in contrast to the baculovirus expression system, do not have kinesin-like proteins. Also described herein are purified kinesins, preferably unglycosylated and methods of use.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1999:194248 HCAPLUS
DOCUMENT NUMBER: 130:233824
TITLE: Plus end-directed microtubule motor protein **CENP-E** required for Xenopus chromosome congression
INVENTOR(S): Wood, Kenneth W.; **Sakowicz, Roman**; Goldstein, Lawrence S. B.; Cleveland, Don W.
PATENT ASSIGNEE(S): The Regents of the University of California, USA
SOURCE: PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9913061	A1	19990318	WO 1998-US19231	19980910
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2303484	AA	19990318	CA 1998-2303484	19980910
AU 9893918	A1	19990329	AU 1998-93918	19980910
AU 745385	B2	20020321		
EP 1012249	A1	20000628	EP 1998-947039	19980910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001526881	T2	20011225	JP 2000-510850	19980910
US 6645748	B1	20031111	US 1998-150867	19980910

PRIORITY APPLN. INFO.: US 1997-58645P P 19970911
WO 1998-US19231 W 19980910

AB The invention provides isolated nucleic acid and amino acid sequences of Xenopus centromere-associated protein-E (XCENP-E), antibodies to XCENP-E, methods of screening for **CENP-E** modulators using biol. active **CENP-E**, and kits for screening for **CENP-E** modulators. The full-length cDNA sequences of XCENP-E encodes a protein of 2954 amino acids with a predicted mol. mass of 340 kDa. XCENP-E is a member of the kinesin superfamily of motor proteins, and consists of a 500-amino acid globular N-terminal domain containing a kinesin-like microtubule motor domain linked to a globular tail domain by a region predicted to form a long, discontinuous α-helical coiled coil. The is the first biol. active **CENP-E** isolated and, surprisingly and contrary to previous reports, it demonstrates a motor that powers chromosome movement toward microtubule plus ends. Using immunodepletion and antibody addition to Xenopus egg exts., the present invention further demonstrates that **CENP-E** plays an essential role in congression.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 4 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 1999:980179 SCISEARCH
THE GENUINE ARTICLE: 255MW
TITLE: The role of the kinetochore protein **CENP-E** in the mitotic checkpoint in xenopus egg extract.
AUTHOR: Abrieu A (Reprint); **Wood K**; Kahana J; Cleveland D W
CORPORATE SOURCE: LUDWIG INST CANC RES, LA JOLLA, CA 92093

COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (NOV 1999) Vol. 10, Supp. [S], pp. 730-730.
Publisher: AMER SOC CELL BIOLOGY, PUBL OFFICE, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
ISSN: 1059-1524.
DOCUMENT TYPE: Conference; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 0

L24 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 1
ACCESSION NUMBER: 1998:680 BIOSIS
DOCUMENT NUMBER: PREV199800000680
TITLE: **CENP-E** is a plus end-directed kinetochore motor required for metaphase chromosome alignment.
AUTHOR(S): Wood, Kenneth W.; **Sakowicz, Roman**; Goldstein, Lawrence S. B.; Cleveland, Don W. [Reprint author]
CORPORATE SOURCE: Lab. Cell Biol., Ludwig Inst. Cancer Res., Univ. California at San Diego, La Jolla, CA 92093-0660, USA
SOURCE: Cell, (Oct. 31, 1997) Vol. 91, No. 3, pp. 357-366. print.
CODEN: CELLB5. ISSN: 0092-8674.
DOCUMENT TYPE: Article
LANGUAGE: English
OTHER SOURCE: Genbank-AF027728; EMBL-AF027728
ENTRY DATE: Entered STN: 23 Dec 1997
Last Updated on STN: 23 Dec 1997

AB Mitosis requires dynamic attachment of chromosomes to spindle microtubules. This interaction is mediated largely by kinetochores. During prometaphase, forces exerted at kinetochores, in combination with polar ejection forces, drive congression of chromosomes to the metaphase plate. A major question has been whether kinetochore-associated microtubule motors play an important role in congression. Using immunodepletion from and antibody addition to Xenopus egg extracts, we show that the kinetochore-associated kinesin-like motor protein **CENP-E** is essential for positioning chromosomes at the metaphase plate. We further demonstrate that **CENP-E** powers movement toward microtubule plus ends in vitro. These findings support a model in which **CENP-E** functions in congression to tether kinetochores to dynamic microtubule plus ends.

	Issue Date	Pages	Document ID
1	20040318	24	US 20040053948 A1
2	20040115	27	US 20040009156 A1
3	20031218	42	US 20030232832 A1
4	20030605	36	US 20030104517 A1
5	20030306	19	US 20030044900 A1
6	20030109	32	US 20030008888 A1
7	20021219	195	US 20020192678 A1
8	20021107	18	US 20020165240 A1
9	20021003	37	US 20020143026 A1
10	20031111	38	US 6645748 B1
11	20030715	46	US 6593098 B1

	Issue Date	Pages	Document ID
12	20030408	74	US 6544766 B1
13	20020625	13	US 6410254 B1

	Issue Date	Pages	Document ID	Title
1	20040318	24	US 20040053948 A1	Compounds, compositions and methods
2	20040115	27	US 20040009156 A1	Antisense therapy using oligonucleotides that target human kinesin genes for treatment of cancer
3	20031218	42	US 20030232832 A1	Pyrrolotriazinone compounds and their use to teat diseases
4	20030605	36	US 20030104517 A1	KINESIN LIGHT CHAIN HOMOLOG
5	20030306	19	US 20030044900 A1	Human kinesins and methods of producing and purifying human kinesins
6	20030109	32	US 20030008888 A1	Novel cyano-substituted dihydropyrimidine compounds and their use to treat diseases
7	20021219	195	US 20020192678 A1	Genes expressed in senescence
8	20021107	18	US 20020165240 A1	Method of treating proliferative diseases using Eg5 inhibitors
9	20021003	37	US 20020143026 A1	Cyano-substituted dihydropyrimidine compounds and their use to treat diseases
10	20031111	38	US 6645748 B1	Plus end-directed microtubule motor required for chromosome congression
11	20030715	46	US 6593098 B1	Genes encoding proteins involved in mitotic checkpoint control and methods of use thereof

	Issue Date	Pages	Document ID	Title
12	20030408	74	US 6544766 B1	Human kinesins and methods of producing and purifying human kinesins
13	20020625	13	US 6410254 B1	Compositions and assays utilizing ADP or phosphate for detecting protein modulators

	Issue Date	Pages	Document ID	Title
1	20040318	617	US 20040052820 A1	Fusion proteins comprising DP-178 and other viral fusion inhibitor peptides useful for treating aids
2	20040304	107	US 20040044184 A1	Cytoskeleton-associated proteins
3	20040304	95	US 20040043037 A1	Staphylococcus aureus polynucleotides and sequences
4	20040219	889	US 20040033235 A1	Nucleic acids encoding DP-178 and other viral fusion inhibitor peptides useful for treating aids
5	20040129	435	US 20040019927 A1	Polynucleotides and polypeptides in plants
6	20031204	125	US 20030224413 A1	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
7	20030911	44	US 20030170866 A1	Novel cyclin-selective ubiquitin carrier polypeptides
8	20030710	30	US 20030127621 A1	Kinesin motor modulators derived from the marine sponge adocia
9	20030501	43	US 20030083261 A1	Class of 12mer peptides that inhibit the function of the mitotic check point protein Mad2
10	20030320	109	US 20030054436 A1	STAPHYLOCOCCUS AUREUS POLYNUCLEOTIDES AND SEQUENCES
11	20030306	19	US 20030044900 A1	Human kinesins and methods of producing and purifying human kinesins

	Issue Date	Pages	Document ID	Title
12	20030102	31	US 20030003466 A1	Artificial mammalian chromosome
13	20020704	49	US 20020086401 A1	Novel cyclin-selective ubiquitin carrier polypeptides
14	20020214	22	US 20020019704 A1	Significance analysis of microarrays
15	20031111	38	US 6645748 B1	Plus end-directed microtubule motor required for chromosome congression
16	20030715	97	US 6593114 B1	Staphylococcus aureus polynucleotides and sequences
17	20030415	70	US 6548290 B1	Geminin gene and protein
18	20030408	74	US 6544766 B1	Human kinesins and methods of producing and purifying human kinesins
19	20030304		US 6528633 B2	Cyclin-selective ubiquitin carrier polypeptides
20	20030211		US 6518013 B1	Methods for the inhibition of epstein-barr virus transmission employing anti-viral peptides capable of abrogating viral fusion and transmission
21	20021203		US 6489134 B1	Kinesin motor modulators derived from the marine sponge Adocia

	Issue Date	Pages	Document ID	Title
22	20021126		US 6485925 B1	Anthrax lethal factor is a MAPK kinase protease
23	20021112		US 6479055 B1	Methods for inhibition of membrane fusion-associated events, including respiratory syncytial virus transmission
24	20020625	13	US 6410254 B1	Compositions and assays utilizing ADP or phosphate for detecting protein modulators
25	20020514		US 6387644 B1	Motor proteins and methods for their use
26	20020219		US 6348353 B1	Artificial mammalian chromosome
27	20020101		US 6335169 B1	Nucleic acids encoding hBub1, a cell cycle checkpoint gene
28	20010508		US 6228983 B1	Human respiratory syncytial virus peptides with antifusogenic and antiviral activities
29	20010327		US 6207403 B1	Kinesin motor modulators derived from the marine sponge Adocia
30	20010130		US 6180379 B1	Cyclin-selective ubiquitin carrier polypeptides
31	20000530		US 6068973 A	Methods for inhibition of membrane fusion-associated events, including influenza virus

	Issue Date	Pages	Document ID	Title
1	20030306	19	US 20030044900 A1	Human kinesins and methods of producing and purifying human kinesins
2	20030408	74	US 6544766 B1	Human kinesins and methods of producing and purifying human kinesins
3	20020514	26	US 6387644 B1	Motor proteins and methods for their use

	L #	Hits	Search Text
1	L1	541	kinesin
2	L2	401010	human
3	L3	248	l1 same l2
4	L4	66	"CENP-E" or "centromere-associated protein-E"
5	L5	13	l3 same l4
6	L6	255738	BERAUD SAKOWICZ-ROMAN OHASHI VAISBERG-EUGENI VAISBERG-EUGENI-A WOOD YU
7	L7	31	l4 and l6
8	L8	67	BERAUD-CHRISTOPHE
9	L9	3	l4 and l8